In the claims:

1. **(currently amended)** A method for use in the analysis of gene or protein expression information, comprising the steps of: [[,]]

~~(a)~~ accessing gene or protein expression data for a number of genes or proteins ~~comprising expression levels of G genes or proteins in S~~ in a number of samples, wherein said data comprises expression levels, and wherein ~~the S~~ said samples ~~may be~~ are classified into [[C]] a number of classes representing cellular states;

~~(b)~~ determining a first measure of ~~the~~ variability of expression levels of ~~each~~ a gene or protein in the for a number of samples; ~~data as a whole; and~~

~~(c)~~ determining a second measure of ~~the~~ variability of expression levels of ~~each~~ a gene or protein within a sample; and ~~each class of sample~~

using the first measure of variability and the second measure of variability in an analysis of gene or protein expression information.

2. **(currently amended)** The method of claim 1, further comprising the step of:

~~(d)~~ determining a between group measure of variability, wherein said between group measure of variability is determined by ~~determining~~ calculating the difference between ~~the~~ said second measure of variability ~~determined in (c) from the~~ and said first measure of variability ~~determined in (b)~~.

3. **(currently amended)** The method of claim 1, further comprising the step of:

generating a comparison of ~~the~~ said first measure of variability ~~determined in (b)~~ to ~~the~~ said second measure[[s]] of variability ~~determined in (c)~~.

4. **(currently amended)** The method of claim 2, further comprising the step of:

generating a comparison of ~~the~~ said second measure of variability ~~determined in (c)~~ to ~~the~~ said between group measure of variability ~~determined in (d)~~.

5. **(currently amended)** The method of claim [[1]] 3, wherein ~~the~~ said comparison comprises determining ~~the~~ a ratio ~~of the measure of variability of (c) to the measure of variability of (b)~~.

6. **(currently amended)** The method of claim 2, wherein ~~the~~ said comparison comprises determining ~~the~~ a ratio ~~of the measure of variability of (c) to the measure of variability of (d)~~.

7. **(currently amended)** The method of claim 3, wherein ~~the~~ said comparison comprises calculating a Wilks' lambda score.

8. **(currently amended)** The method of claim 3, wherein ~~the~~ said comparison comprises scaling the first measure of variability ~~of (b)~~ by the second measure of variability ~~of (c)~~.

9. **(currently amended)** The method of claim 1, wherein ~~the~~ said first measure of variability is selected from the group consisting of[[:]] variance and kurtosis; and wherein said second measure of variability is selected from the group consisting of variance and kurtosis.

10. **(currently amended)** The method of claim 1, wherein [[G]] said number of genes or proteins is one.

11. **(currently amended)** The method of claim 1, wherein [[G]] said number of genes or proteins is two or greater.

12. **(currently amended)** The method of claim 1, wherein [[C]] said number of classes is two or greater, and wherein [[S]] said number of genes or protiens is equal to or greater than [[C]] said number of classes.

13. **(original)** The method of claim 1, wherein the data is organized into a data matrix X_k for each class k, and wherein each data matrix is organized such that $X(i,j)$ is the expression of gene j in sample i.

14. **(currently amended)** The method of claim 2, wherein ~~the~~ said second measure of variability ~~determined in (c)~~ is represented by a matrix $\boldsymbol{B}$, and wherein said between group measure of variability ~~determined in (d)~~ is represented by a matrix $\boldsymbol{W}$.

15. **(original)** The method of claim 14, wherein $\boldsymbol{W}$ is generated according to the formula

$$\boldsymbol{W} = \sum_{k=1}^{c} \left(\boldsymbol{X}_k - \boldsymbol{1}\overline{\boldsymbol{x}}_k\right)^T \left(\boldsymbol{X}_k - \boldsymbol{1}\overline{\boldsymbol{x}}_k\right)$$

wherein $\overline{\mathbf{x}}_k$ is the group mean $(1 \times g)$ for class k.

16. **(original)** The method of claim 14, wherein $\boldsymbol{B}$ is generated according to the formula

$$\boldsymbol{B} = \boldsymbol{T} - \boldsymbol{W} = \left(\mathbf{X} - \mathbf{1}\overline{\mathbf{x}}\right)^T \left(\mathbf{X} - \mathbf{1}\overline{\mathbf{x}}\right) - \mathbf{W}$$

wherein $\overline{\mathbf{x}}_k$ is the group mean $(1 \times g)$ for class k, $\overline{\mathbf{x}}$ is the mean for all the data, and $\boldsymbol{T}$ is the total variance of all the data..

17. **(original)** The method of claim 14, comprising generating a comparison of the matrix $\boldsymbol{B}$ and the matrix $\boldsymbol{W}$.

18. **(original)** The method of claim 17, wherein the comparison is a matrix $\boldsymbol{W}^{1}\boldsymbol{B}$.

19. **(currently amended)** The method of claim 17, further comprising the step of:

maximizing the separation between ~~the~~ said classes in a reduced dimensional space.

20. **(currently amended)** The method of claim 19, wherein maximizing the separation between ~~the~~ said classes in a reduced dimensional space comprises generating an eigenvector matrix $\boldsymbol{L}$ of the matrix $\boldsymbol{W}^{1}\boldsymbol{B}$ and an eigenvalue matrix Λ of the matrix $\boldsymbol{W}^{1}\boldsymbol{B}$.

21. **(original)** The method of claim 20, wherein a column of $\boldsymbol{L}$ defines a discriminant function of the reduced dimensional space, and wherein each entry in the column indicates the contribution of each gene to the discriminant function.

22. **(currently amended)** The method of claim 19, wherein the variance-covariance structure is ~~similar~~ substantially similar in each class.

23. **(currently amended)** The method of claim 19, wherein maximizing the separation between ~~the~~ said classes in a reduced dimensional space comprises generating a singular value decomposition of the matrix $\boldsymbol{W}^{1}\boldsymbol{B}$.

24. **(currently amended)** The method of claim 23, wherein generating [[a]] said singular value decomposition of the matrix $\boldsymbol{W}^{1}\boldsymbol{B}$ is performed according to the formula:

$$\mathbf{W}^{-1}\mathbf{B} = \mathbf{U}\Lambda\mathbf{L}^{T}$$

wherein $\boldsymbol{U}$ is a left singular vector, $\boldsymbol{L}$ is a matrix of discriminant functions, and Λ is a matrix of singular values representing the discriminant loadings in the corresponding functions.

25. **(currently amended)** The method of claim 21, further comprising the step of:

calculating a discriminator vector for each sample i, wherein the discriminator vector represents a position of the sample in the reduced dimensional space.

26. **(currently amended)** The method of claim 25, wherein calculating [[a]] said discriminator vector comprises operating the formula:

$$y_j = \boldsymbol{i}\boldsymbol{L}_j = \sum_{z=1}^{g} i_z L_{ij}$$

wherein y_j is the discriminator score of the sample $\boldsymbol{i}$ (a sample of g genes) for each column j of matrix $\boldsymbol{L}$, and wherein the discriminator vector is a combination of each y_j into a vector having a dimensionality that is equal to the number of dimensions in the reduced dimensional space.

27. **(currently amended)** The method of claim 3, further comprising the step of:

generating discriminant loadings based on ~~the~~ said comparison.

28. **(currently amended)** The method of claim 4, further comprising the step of:

generating discriminant loadings based on ~~the~~ said comparison.

29. **(currently amended)** The method of claim 27, further comprising the step of:

generating a discriminator vector for each sample, wherein the discriminator vector describes a point in a space having one or more dimensions.

30. **(currently amended)** The method of claim 28, further comprising the step of:

generating a discriminator vector for each sample based on the comparison, wherein the discriminator vector describes a point in a space having one or more dimensions.

31. **(currently amended)** The method of claim 27, further comprising the step of:

determining the contribution of ~~the~~ said expression levels of a gene or protein to ~~the~~ said discriminant loadings~~, wherein a gene or protein that contributes significantly to a dimension is a gene or protein that is related to a cellular state of one or more sample~~.

32. **(currently amended)** The method of claim 28, further comprising the step of:

determining the contribution of ~~the~~ said expression levels of a gene or protein to ~~the~~ said discriminant loadings~~, wherein a gene or protein that contributes significantly to a dimension is a gene or protein that is related to a cellular state or a change in cellular state of one or more sample~~.

33. **(currently amended)** The method of claim 31, wherein [[C]] said number of classes is two or greater ~~and the space has C-1 dimensions~~.

34. **(currently amended)** The method of claim 32, further comprising the step of:

generating a rank order list of said genes or proteins based on said contribution ~~to the dimensions of the space~~.

35. **(currently amended)** The method of claim 34, wherein ~~the~~ said rank order list is generated by calculating and comparing the F score for each gene or protein, wherein an F score may be calculated via transformation of a Wilks' lambda score.

Claims 36-45 **(canceled)**

46. **(currently amended)** A computer product for use in analyzing gene or protein expression data, the product disposed on a computer readable medium, and comprising instructions for causing a processor to:

accessing gene or protein expression data for a number of genes or proteins in a number of samples, wherein said data comprises expression levels, and wherein said samples are classified into a number of classes representing cellular states;

~~(a)~~ determine a first measure of the variability of expression levels of each gene or protein in the data as a whole; ~~and~~

~~(b)~~ determine a second measure of the variability of expression levels of each gene or protein within each ~~class of~~ sample; and

use the first measure of variability and the second measure of variability in the analysis of gene or protein expression information.

47. **(currently amended)** The computer product of claim 46, further comprising instructions for causing a processor to:

generate for ~~the~~ said gene or protein a comparison of the first measure of variability ~~determined in (b)~~ to the second measure[[s]] of variability ~~determined in (c)~~.

48. **(currently amended)** A system comprising a processor and instructions for causing a processor to:

accessing gene or protein expression data for a number of genes or proteins in a number of samples, wherein said data comprises expression levels, and wherein said samples are classified into a number of classes representing cellular states;

~~(a)~~ determine a first measure of the variability of expression levels of each gene or protein in the data as a whole; ~~and~~

~~(b)~~ determine a second measure of the variability of expression levels of each gene or protein within each ~~class of~~ sample; and

use the first measure of variability and the second measure of variability in the analysis of gene or protein expression information.

Claims 49-73 **(canceled)**